WHAT IS CLAIMED IS:

| 1 | An isolated infectious chimeric respiratory syncytial virus (RSV) |
|---|---|
| 2 | comprising a major nucleocapsid (N) protein, a nucleocapsid phosphoprotein (P), a large |
| 3 | polymerase protein (L), a RNA polymerase elongation factor, and a partial or complete |
| 4 | RSV background genome or antigenome of a human or bovine RSV combined with one |
| 5 | or more heterologous gene(s) and/or genome segment(s) of a different RSV to form a |
| 6 | human-bovine chimeric RSV genome or antigenome. |
| 1 | 2. The chimeric RSV of claim 1, wherein said one or more |
| 2 | heterologous gene(s) and/or genome segment(s) include one or more RSV NS1, NS2, N, |
| 3 | P, M, SH, M2(ORF1), M2(ORF2), L, F or G gene(s) or genome segment(s) or a leader, |
| 4 | trailer or intergenic region of the RSV genome or a segment thereof. |
| 1 | 3. The chimeric RSV of claim 2, wherein said one or more |
| 2 | heterologous gene(s) and/or genome segment(s) includes one or more gene(s) or genome |
| 3 | segment(s) encoding a RSV F, G and/or SH glycoprotein or an immunogenic domain or |
| 4 | epitope thereof. |
| 1 | 4. The chimeric RSV of claim 1, wherein the human-bovine chimeric |
| 2 | RSV genome or antigenome encodes a chimeric glycoprotein having both human and |
| 3 | bovine glycoprotein domains or immunogenic epitopes. |
| 1 | 5. The chimeric RSV of claim 4, wherein said one or more |
| 2 | heterologous gene(s) and/or genome segment(s) includes a gene segment encoding a |
| 3 | glycoprotein ectodomain. |
| 1 | 6. The chimeric RSV of claim 1, wherein a heterologous gene or |
| 2 | genome segment is substituted for a counterpart gene or genome segment in a partial RSV |
| 3 | background genome or antigenome. |
| 1 | 7. The chimeric RSV of claim 1, wherein a heterologous gene or |
| 2 | genome segment is added adjacent to, within, or as a replacement to, a noncoding region |
| 3 | of the partial or complete RSV background genome or antigenome. |

10030951.070102 PCT/US00/17755

| 1 | 8. The chimeric RSV of claim 1, wherein a heterologous gene or |
|---|--|
| 2 | genome segment is added or substituted at a position corresponding to a wild-type gene |
| 3 | order position of a counterpart gene or genome segment within the partial or complete |
| 4 | RSV background genome or antigenome. |
| 1 | 9. The chimeric RSV of claim 1, wherein a heterologous gene or |
| 1 | genome segment is added or substituted at a position that is more promoter-proximal or |
| 2 | - |
| 3 | promoter-distal compared to a wild-type gene order position of a counterpart gene or |
| 4 | genome segment within the partial or complete RSV background genome or antigenome. |
| 1 | 10. The chimeric RSV of claim 1, wherein the chimeric genome or |
| 2 | antigenome comprises a partial or complete human RSV background genome or |
| 3 | antigenome combined with one or more heterologous gene(s) and/or genome segment(s) |
| 4 | from a bovine RSV. |
| 1 | 11. The chimeric RSV of claim 10, wherein one or more genes selected |
| | from N, P, NS1, NS2, M2-1 and M of a human RSV is/are replaced by one or more |
| 2 | |
| 3 | heterologous gene(s) from a bovine RSV. |
| 1 | 12. The chimeric RSV of claim 11, wherein both N and P genes of a |
| 2 | human RSV are replaced by counterpart N and P genes from a bovine RSV. |
| 1 | 13. The chimeric RSV of claim 11, wherein both NS1 and NS2 genes |
| 2 | of a human RSV are replaced by counterpart NS1 and NS2 genes from a bovine RSV. |
| _ | of a name its valo replaced by commercial and its general actions and |
| 1 | 14. The chimeric RSV of claim 11, wherein two or more of the M2-1, |
| 2 | M2-2 and L genes are replaced by counterpart genes from a bovine RSV |
| 1 | 15. The chimeric RSV of claim 11, wherein each of the N, P, NS1, |
| | NS2, M2-1 and M genes of a human RSV are replaced by counterpart N, P, NS1, NS2, |
| 2 | |
| 3 | M2-1 and M genes from a bovine RSV. |
| 1 | 16. The chimeric RSV of claim 1, wherein the chimeric genome or |
| 2 | antigenome comprises a partial or complete bovine RSV background genome or |
| 3 | antigenome combined with one or more heterologous gene(s) and/or genome segment(s) |
| 4 | from a human RSV. |
| | |



| 1 | 17. The chimeric RSV of claim 16, wherein one or more human RSV |
|---|---|
| 2 | glycoprotein genes selected from F, G and SH, or one or more genome segment(s) |
| 3 | encoding cytoplasmic domain, transmembrane domain, ectodomain or immunogenic |
| 4 | epitope portion(s) of F, G, and/or SH is/are added or substituted within a partial or |
| 5 | complete bovine RSV background genome or antigenome. |
| 1 | 18. The chimeric RSV of claim 17, wherein one or both human RSV |
| 2 | glycoprotein genes F and G is/are substituted to replace one or both counterpart F and G |
| 3 | glycoprotein genes in a partial bovine RSV background genome or antigenome. |
| 1 | 19. The chimeric RSV of claim 17, wherein the human-bovine |
| 2 | chimeric genome or antigenome incorporates antigenic determinants from one or both |
| 3 | subgroup A and subgroup B human RSV. |
| 1 | 20. The chimeric RSV of claim 17, wherein both human RSV |
| 2 | glycoprotein genes F and G are substituted to replace counterpart F and G glycoprotein |
| 3 | genes in the bovine RSV background genome or antigenome. |
| _ | |
| 1 | 21. The chimeric RSV of claim 20, which is rBRSV/A2. |
| 1 | 22. The chimeric RSV of claim 9, wherein one or more human RSV |
| 2 | glycoprotein genes selected from F, G and SH is/are added or substituted at a position that |
| 3 | is more promoter-proximal compared to a wild-type gene order position of a counterpart |
| 4 | gene or genome segment within a partial or complete bovine RSV background genome of |
| 5 | antigenome. |
| 1 | 23. The chimeric RSV of claim 22, wherein both human RSV |
| 2 | glycoprotein genes G and F are substituted at gene order positions 1 and 2, respectively, |
| 3 | to replace counterpart G and F glycoprotein genes deleted at wild type positions 7 and 8, |
| 4 | respectively in a partial bovine RSV background genome or antigenome. |
| 1 | 24. The chimeric RSV of claim 23, which is rBRSV/A2-G1F2 |
| 1 | 25. The chimeric RSV of claim 17, wherein the chimeric genome or |
| 2 | antigenome is further modified by addition or substitution of one or more additional |
| 3 | heterologous gene(s) or genome segment(s) from a human RSV within the partial or |
| | |

1

2

3

4

1

2

3

1

- complete bovine background genome or antigenome to increase genetic stability or alter attenuation, reactogenicity or growth in culture of the chimeric virus.
- 1 26. The chimeric RSV of claim 16, wherein one or more human RSV envelope-associated genes selected from F, G, SH, and M is/are added or substituted within a partial or complete bovine RSV background genome or antigenome.
 - 27. The chimeric RSV of claim 26, wherein one or more human RSV envelope-associated genes selected from F, G, SH, and M is/are added or substituted within a partial bovine RSV background genome or antigenome in which one or more envelope-associated genes selected from F, G, SH, and M is/are deleted.
 - 28. The chimeric RSV of claim 27, wherein human RSV envelope-associated genes F, G, and M are added within a partial bovine RSV background genome or antigenome in which envelope-associated genes F, G, SH, and M are deleted.
 - 29. The chimeric RSV of claim 28, which is rBRSV/A2-MGF.
- antigenome incorporates at least one and up to a full complement of attenuating mutations present within a panel of mutant human RSV strains, said panel comprising cpts RSV 248 (ATCC VR 2450), cpts RSV 248/404 (ATCC VR 2454), cpts RSV 248/955 (ATCC VR 2453), cpts RSV 530 (ATCC VR 2452), cpts RSV 530/1009 (ATCC VR 2451), cpts RSV 530/1030 (ATCC VR 2455), RSV B-1 cp52/2B5 (ATCC VR 2542), and RSV B-1 cp-23 (ATCC VR 2579).
- 1 31. The chimeric RSV of claim 30, wherein the chimeric genome or 2 antigenome incorporates attenuating mutations adopted from different mutant RSV 3 strains.
- The chimeric RSV of claim 1, wherein the chimeric genome or antigenome incorporates at least one and up to a full complement of attenuating mutations specifying an amino acid substitution at Val267 in the RSV N gene, Glu218 and/or Thr523 in the RSV F gene, Asn43, Cys319, Phe 521, Gln831, Met1169, Tyr1321 and/or His 1690 in the RSV polymerase gene L, and a nucleotide substitution in the gene-start sequence of gene M2.

The chimeric RSV of claim 32, wherein the chimeric genome or 33. 1 antigenome incorporates at least two attenuating mutations. 2 The chimeric RSV of claim 32, wherein the chimeric genome or 34. 1 antigenome includes at least one attenuating mutation stabilized by multiple nucleotide 2 changes in a codon specifying the mutation. 3 The chimeric RSV of claim 1, wherein the chimeric genome or 35. 1 antigenome further comprises a nucleotide modification specifying a phenotypic change 2 selected from a change in growth characteristics, attenuation, temperature-sensitivity, 3 cold-adaptation, plaque size, host-range restriction, or a change in immunogenicity. 4 The chimeric RSV of claim 35, wherein the nucleotide 36. 1 modification alters a SH, NS1, NS2, M2ORF2, or G gene of the chimeric virus. 2 37. The chimeric RSV of claim 36, wherein a SH, NS1, NS2, M2 1 ORF2, or G gene of the chimeric virus is deleted in whole or in part or expression of the 2 gene is ablated by introduction of one or more stop codons in an open reading frame of 3 4 the gene. The chimeric RSV of claim 35, wherein the nucleotide 38. 1 modification comprises a nucleotide deletion, insertion, substitution, addition or 2 rearrangement of a cis-acting regulatory sequence of a selected gene within the chimeric 3 RSV genome or antigenome. 4 39. The chimeric RSV of claim 38, wherein a gene end (GE) signal of 1 the NS1 or NS2 gene is modified. 2 The chimeric RSV of claim 35, wherein the nucleotide 1 40. 2 modification comprises an insertion, deletion, substitution, or rearrangement of a 3 translational start site within the chimeric genome or antigenome. 41. The chimeric RSV of claim 40, wherein the translational start site 1 2 for a secreted form of the RSV G glycoprotein is ablated.

antigenome is modified to encode a non-RSV molecule selected from a cytokine, a T-

The chimeric RSV of claim 35, wherein the chimeric genome or

42.

1.

2

100Z0951 O70102

PCT/US00/17755 WO 01/04335

- helper epitope, a restriction site marker, or a protein of a microbial pathogen capable of 3 eliciting a protective immune response in a mammalian host. 4 The chimeric RSV of claim 35, which incorporates one or more 43. 1 gene(s) and/or genome segment(s) from parainfluenza virus (PIV). 2 The chimeric RSV of claim 43, wherein the chimeric genome or 44. 1 antigenome encodes a PIV HN or F glycoprotein or immunogenic domain or epitope 2 3 thereof. The chimeric RSV of claim 44, wherein the chimeric genome or 45. 1 antigenome encodes an ectodomain or immunogenic epitope of HN or F of PIV1, PIV2, 2 or PIV3. 3 The chimeric RSV of claim 1 which is a virus. 46. 1 The chimeric RSV of claim 1 which is a subviral particle. 47. 1 A method for stimulating the immune system of an individual to 48. 1 induce protection against RSV which comprises administering to the individual an 2 immunologically sufficient amount of the chimeric RSV of claim 1 combined with a 3 physiologically acceptable carrier. 4 The method of claim 48, wherein the chimeric RSV is administered 49. 1 in a dose of 10^3 to 10^6 PFU. 2 The method of claim 48, wherein the chimeric RSV is administered 50. 1 2 to the upper respiratory tract. The method of claim 48, wherein the chimeric RSV is administered 51. 1 2 by spray, droplet or aerosol. The method of claim 48, wherein the chimeric RSV is administered 52. 1 to an individual seronegative for antibodies to RSV or possessing transplacentally 2 acquired maternal antibodies to RSV. 3
- The method of claim 48, wherein the chimeric RSV elicits an 1 53. immune response against either human RSV A or RSV B. 2

| l | 54. The method of claim 48, wherein the chimeric RSV elicits an |
|---|---|
| 2 | immune response against both human RSV A and RSV B. |
| | and the stimulian DCV aligits an |
| 1 | 55. The method of claim 48, wherein the chimeric RSV elicits an |
| 2 | immune response against either human RSV A or RSV B and is co-administered with an |
| 3 | immunologically sufficient amount of a second attenuated RSV capable of eliciting an |
| 4 | immune response against human RSV A or RSV B, whereby an immune response is |
| 5 | elicited against both human RSV A and RSV B. |
| | 56. The method of claim 55, wherein the chimeric RSV and second |
| 1 | |
| 2 | attenuated RSV are administered simultaneously as a mixture. |
| 1 | 57. An immunogenic composition to elicit an immune response against |
| 2 | RSV comprising an immunologically sufficient amount of the chimeric RSV of claim 1 in |
| 3 | a physiologically acceptable carrier. |
| , | |
| 1 | 58. The immunogenic composition of claim 57, formulated in a dose of |
| 2 | 10 ³ to 10 ⁶ PFU. |
| 1 | 59. The immunogenic composition of claim 57, formulated for |
| 1 | administration to the upper respiratory tract by spray, droplet or aerosol. |
| 2 | |
| 1 | 60. The immunogenic composition of claim57, wherein the chimeric |
| 2 | RSV elicits an immune response against either human RSV A or RSV B. |
| | |
| 1 | 61. The immunogenic composition of claim 57, wherein the chimeric |
| 2 | RSV elicits an immune response against both human RSV A and RSV B |
| 1 | 62. The immunogenic composition of claim 57, wherein the chimeric |
| 2 | RSV elicits an immune response against either human RSV A or RSV B and wherein the |
| 3 | composition further comprises an immunologically sufficient amount of a second |
| | attenuated RSV capable of eliciting an immune response against human RSV A or RSV |
| 4 | B, whereby the composition elicits an immune response against both human RSV A and |
| 5 | |
| 6 | RSV B. |
| 1 | 63. An isolated polynucleotide molecule comprising a chimeric RSV |
| 2 | genome or antigenome which includes a partial or complete RSV background genome or |

2



- 3 antigenome of a human or bovine RSV combined with one or more heterologous gene(s) 4 or genome segment(s) of a different RSV to form a human-bovine chimeric RSV genome 5 or antigenome. The isolated polynucleotide of claim 63, wherein said one or more 1 64. heterologous gene(s) and/or genome segment(s) include one or more RSV NS1, NS2, N, 2 3 P, M, SH, M2(ORF1), M2(ORF2), L, F or G gene(s) or genome segment(s) or a leader, trailer or intergenic region of the RSV genome or a segment thereof. 4 1 65. The isolated polynucleotide of claim 63, wherein a heterologous 2 gene or genome segment is substituted for a counterpart gene or genome segment in a partial RSV background genome or antigenome. 3 66. The isolated polynucleotide of claim 63, wherein a heterologous 1 2 gene or genome segment is added adjacent to, within, or as a replacement to, a noncoding 3 region of the partial or complete RSV background genome or antigenome. 1 67. The isolated polynucleotide of claim 63, wherein a heterologous 2 gene or genome segment is added or substituted at a position that is more promoterproximal or promoter-distal compared to a wild-type gene order position of a counterpart 3 gene or genome segment within the partial or complete RSV background genome or 4 5 antigenome. 1 68. The isolated polynucleotide of claim 63, wherein the chimeric 2 genome or antigenome comprises a partial or complete human RSV background genome or antigenome combined with one or more heterologous gene(s) and/or genome 3 4 segment(s) from a bovine RSV. 1 The isolated polynucleotide of claim 68, wherein one or more 69.
- 1 70. The isolated polynucleotide of claim 68, wherein both N and P genes of a human RSV are replaced by counterpart N and P genes from a bovine RSV.

or more heterologous gene(s) from a bovine RSV.

genes selected from N, P, NS1, NS2, M2-1 and M of a human RSV is/are replaced by one



| 1 | 71. The isolated polynucleotide of claim 68, wherein both NS1 and |
|---|---|
| 2 | NS2 genes of a human RSV are replaced by counterpart NS1 and NS2 genes from a |
| 3 | bovine RSV. |
| 1 | 72. The isolated polynucleotide of claim 68, wherein two or more of |
| 2 | the M2-1, M2-2 and L genes are replaced by counterpart genes from a bovine RSV |
| 1 | 73. The isolated polynucleotide of claim 63, wherein the chimeric |
| 2 | genome or antigenome comprises a partial or complete bovine RSV background genome |
| 3 | or antigenome combined with one or more heterologous gene(s) and/or genome |
| 4 | segment(s) from a human RSV. |
| 1 | 74. The isolated polynucleotide of claim 73, wherein one or more |
| 2 | human RSV glycoprotein genes selected from F, G and SH, or one or more genome |
| 3 | segment(s) encoding cytoplasmic domain, transmembrane domain, ectodomain or |
| 4 | immunogenic epitope portion(s) of F, G, and/or SH is/are added or substituted within a |
| 5 | partial or complete bovine RSV background genome or antigenome. |
| 1 | 75. The isolated polynucleotide of claim 74, wherein one or both |
| 2 | human RSV glycoprotein genes F and G is/are substituted to replace one or both |
| 3 | counterpart F and G glycoprotein genes in a partial bovine RSV background genome or |
| 4 | antigenome. |
| 1 | 76. The isolated polynucleotide of claim 75, wherein both human RSV |
| 2 | glycoprotein genes F and G are substituted to replace counterpart F and G glycoprotein |
| 3 | genes in the bovine RSV background genome or antigenome. |
| 1 | 77. The isolated polynucleotide of claim 67, wherein one or more |
| 2 | human RSV glycoprotein genes selected from F, G and SH is/are added or substituted at a |
| 3 | position that is more promoter-proximal compared to a wild-type gene order position of a |
| 4 | counterpart gene or genome segment within a partial or complete bovine RSV |
| 5 | background genome or antigenome. |
| 1 | 78. The isolated polynucleotide of claim 77, wherein both human RSV |
| 2 | glycoprotein genes G and F are substituted at gene order positions 1 and 2, respectively, |

10030051 070102

PCT/US00/17755

WO 01/04335

to replace counterpart G and F glycoprotein genes deleted at wild type positions 7 and 8,
 respectively in a partial bovine RSV background genome or antigenome.

- The isolated polynucleotide of claim 73, wherein the chimeric genome or antigenome is further modified by addition or substitution of one or more additional heterologous gene(s) or genome segment(s) from a human RSV within the partial or complete bovine background genome or antigenome to increase genetic stability or alter attenuation, reactogenicity or growth in culture of the chimeric virus.
- 1 80. The isolated polynucleotide of claim 73, wherein one or more 2 human RSV envelope-associated genes selected from F, G, SH, and M is/are added or 3 substituted within a partial or complete bovine RSV background genome or antigenome.
- 1 81. The isolated polynucleotide of claim 80, wherein human RSV
 2 envelope-associated genes F, G, and M are added within a partial bovine RSV
 3 background genome or antigenome in which envelope-associated genes F, G, SH, and M
 4 are deleted.
- 1 82. The isolated polynucleotide molecule of claim 63, wherein the
 2 human-bovine chimeric genome or antigenome incorporates antigenic determinants from
 3 both subgroup A and subgroup B human RSV.
 - 83. The isolated polynucleotide molecule of claim 63, wherein the chimeric genome or antigenome is further modified by incorporation of one or more attenuating mutations.

1

2

3

- 1 84. The isolated polynucleotide molecule of claim 63, further
 2 comprising a nucleotide modification specifying a phenotypic change selected from a
 3 change in growth characteristics, attenuation, temperature-sensitivity, cold-adaptation,
 4 plaque size, host-range restriction, or a change in immunogenicity.
- 1 85. The isolated polynucleotide molecule of claim 63, wherein a SH, 2 NS1, NS2, M2ORF2, or G gene is modified.
- 1 86. The isolated polynucleotide molecule of claim 85, wherein the SH, 2 NS1, NS2, M2 ORF2, or G gene is deleted in whole or in part or expression of the gene is 3 ablated by introduction of one or more stop codons in an open reading frame of the gene.

ingingi office

WO 01/04335

PCT/US00/17755

| 1 | 87. The isolated polynucleotide molecule of claim 59, wherein the |
|---|--|
| 2 | nucleotide modification comprises a nucleotide deletion, insertion, addition or |
| 3 | rearrangement of a cis-acting regulatory sequence of a selected RSV gene within the |
| 4 | chimeric RSV genome or antigenome. |
| _ | |
| 1 | 88. A method for producing an infectious attenuated chimeric RSV |
| 2 | particle from one or more isolated polynucleotide molecules encoding said RSV, |
| 3 | comprising: |
| 4 | expressing in a cell or cell-free lysate an expression vector comprising an |
| 5 | isolated polynucleotide comprising a partial or complete RSV background genome or |
| 6 | antigenome of a human or bovine RSV combined with one or more heterologous gene(s) |
| 7 | or genome segment(s) of a different RSV to form a human-bovine chimeric RSV genome |
| 8 | or antigenome, and RSV N, P, L and RNA polymerase elongation factor proteins. |
| _ | |
| 1 | 89. The method of claim 88, wherein the chimeric RSV genome or |
| 2 | antigenome and the N, P, L and RNA polymerase elongation factor proteins are expressed |
| 3 | by two or more different expression vectors. |
| 1 | 90. The chimeric RSV of claim 1, wherein the bovine-human chimeric |
| 2 | genome or antigenome comprises a partial or complete RSV vector genome or |
| 3 | antigenome combined with one or more heterologous genes or genome segments |
| 4 | encoding one or more antigenic determinants of one or more heterologous pathogens. |
| _ | |
| 1 | 91. The chimeric RSV of claim 90, wherein said one or more |
| 2 | heterologous pathogens is a heterologous RSV and said heterologous gene(s) or genome |
| 3 | segment(s) encode(s) one or more RSV NS1, NS2, N, P, M, SH, M2(ORF1), M2(ORF2), |
| 4 | L, F or G protein(s) or fragment(s) thereof. |
| 1 | 92. The chimeric RSV of claim 90, wherein the vector genome or |
| 2 | antigenome is a partial or complete RSV A genome or antigenome and the heterologous |
| 3 | gene(s) or genome segment(s) encoding the antigenic determinant(s) is/are of a RSV B |
| 4 | subgroup virus. |
| | • |

10030951 070108

WO 01/04335

PCT/US00/17755

| 1 | 93. The chimeric RSV of claim 90, wherein the chimeric genome or |
|---|---|
| 2 | antigenome incorporates one or more gene(s) or genome segment(s) of a BRSV that |
| 3 | specifies attenuation. |
| 1 | 94. The chimeric RSV of claim 90, wherein one or more HPIV1, |
| 2 | HPIV2, or HPIV3 gene(s) or genome segment(s) encoding one or more HN and/or F |
| 3 | glycoprotein(s) or antigenic domain(s), fragment(s) or epitope(s) thereof is/are added to |
| 4 | or incorporated within the partial or complete HRSV vector genome or antigenome. |
| 1 | 95. The chimeric RSV of claim 90, wherein a transcription unit |
| 2 | comprising an open reading frame (ORF) of an HPIV2 HN or F gene is added to or |
| 3 | incorporated within the chimeric HRSV vector genome or antigenome. |
| 1 | 96. The chimeric RSV of claim 35, wherein the vector genome or |
| 2 | antigenome is a partial or complete BRSV genome or antigenome and the heterologous |
| 3 | gene(s) or genome segment(s) encoding the antigenic determinant(s) is/are of one or more |
| 4 | HRSV(s). |
| | |
| 1 | 97. The chimeric RSV of claim 96, wherein the partial or complete |
| 2 | BRSV genome or antigenome incorporates one or more gene(s) or genome segment(s) |
| 3 | encoding one or more HRSV glycoprotein genes selected from F, G and SH, or one or |
| 4 | more genome segment(s) encoding cytoplasmic domain, transmembrane domain, |
| 5 | ectodomain or immunogenic epitope portion(s) of F, G, and/or SH of HRSV. |
| l | 98. The chimeric RSV of claim 90, wherein the vector genome or |
| 2 | antigenome is a partial or complete HRSV or BRSV genome or antigenome and the |
| 3 | heterologous pathogen is selected from measles virus, subgroup A and subgroup B |
| 1 | respiratory syncytial viruses, mumps virus, human papilloma viruses, type 1 and type 2 |
| 5 | human immunodeficiency viruses, herpes simplex viruses, cytomegalovirus, rabies virus, |
| 5 | Epstein Barr virus, filoviruses, bunyaviruses, flaviviruses, alphaviruses and influenza |
| 7 | viruses. |
| l | 99. The chimeric RSV of claim 98, wherein said one or more |
| 2 | heterologous antigenic determinant(s) is/are selected from measles virus HA and F |
| 3 | proteins, subgroup A or subgroup B respiratory syncytial virus F, G, SH and M2 proteins, |
| | |



- 4 mumps virus HN and F proteins, human papilloma virus L1 protein, type 1 or type 2
- 5 human immunodeficiency virus gp160 protein, herpes simplex virus and cytomegalovirus
- 6 gB, gC, gD, gE, gG, gH, gI, gJ, gK, gL, and gM proteins, rabies virus G protein, Epstein
- 7 Barr Virus gp350 protein; filovirus G protein, bunyavirus G protein, Flavivirus E and
- 8 NS1 proteins, and alphavirus E protein, and antigenic domains, fragments and epitopes
- 9 thereof.
- 1 100. The chimeric RSV of claim 99, wherein the heterologous pathogen
- 2 is measles virus and the heterologous antigenic determinant(s) is/are selected from the
- 3 measles virus HA and F proteins and antigenic domains, fragments and epitopes thereof.
- 1 101. The chimeric RSV of claim 100, wherein a transcription unit
- 2 comprising an open reading frame (ORF) of a measles virus HA gene is added to or
- 3 incorporated within a HRSV vector genome or antigenome.